SEQUENCE LISTING

5

10

- (i) APPLICANT:
 - (A) NAME: Akzo nobel n.v.
 - (B) STREET: Velperweg 76
 - (C) CITY: Arnhem
 - (E) COUNTRY: The Netherlands
 - (F) POSTAL CODE (ZIP): 6824 BM
 - (G) TELEPHONE: 0412-666379
 - (H) TELEFAX: 0412-650592
 - (I) TELEX: 37503 akpha nl

15

- (ii) TITLE OF INVENTION: Novel estrogen receptor
- (iii) NUMBER OF SEQUENCES: 28

20

- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

-45

- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAATTACA GCATTCCCAG CAATGTCACT AACTTGGAAG GTGGGCCTGG TCGGCAGACC 60 ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC 120 CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA 180 GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC 240 GCCAGCCCTG TTACTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC 300 GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT 360 AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC 420 GATAAAAACC GGCGCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA 480 ATGGTGAAGT GTGGCTCCCG GAGAGAGAGA TGTGGGTACC GCCTTGTGCG GAGACAGAGA AGTGCCGACG AGCAGCTGCA CTGTGCCGGC AAGGCCAAGA GAAGTGGCGG CCACGCGCCC 600 CGAGTGCGGG AGCTGCTGCT GGACGCCCTG AGCCCCGAGC AGCTAGTGCT CACCCTCCTG 660 GAGGCTGAGC CGCCCCATGT GCTGATCAGC CGCCCCAGTG CGCCCTTCAC CGAGGCCTCC 720 ATGATGATGT CCCTGACCAA GTTGGCCGAC AAGGAGTTGG TACACATGAT CAGCTGGGCC 780 AAGAAGATTC CCGGCTTTGT GGAGCTCAGC CTGTTCGACC AAGTGCGGCT CTTGGAGAGC 840 TGTTGGATGG AGGTGTTAAT GATGGGGCTG ATGTGGCGCT CAATTGACCA CCCCGGCAAG 900 CTCATCTTTG CTCCAGATCT TGTTCTGGAC AGGGATGAGG GGAAATGCGT AGAAGGAATT 960 CTGGAAATCT TTGACATGCT CCTGGCAACT ACTTCAAGGT TTCGAGAGTT AAAACTCCAA 1020 1080 CACAAAGAAT ATCTCTGTGT CAAGGCCATG ATCCTGCTCA ATTCCAGTAT GTACCCTCTG GTCACAGCGA CCCAGGATGC TGACAGCAGC CGGAAGCTGG CTCACTTGCT GAACGCCGTG 1140

20

30

ACCGATGCTT TGGTTTGGGT GATTGCCAAG AGCGGCATCT CCTCCCAGCA GCAATCCATG 1200

CGCCTGGCTA ACCTCCTGAT GCTCCTGTCC CACGTCAGGC ATGCGAGGTAA CAAGGGCATG 1260

GAACATCTGC TCAACATGAA GTGCAAAAAT GTGGTCCCAG TGTATGACCT GCTGCTGGAG 1320

ATGCTGAATG CCCACGTGCT TCGCGGGTGC AAGTCCTCCA TCACGGGGTC CGAGTGCAGC 1380

CCGGCAGAGG ACAGTAAAAG CAAAGAGGGC TCCCAGAACC CACAGTCTCA GTGA 1434

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1251 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

30

35

5

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

60 ATGAATTACA GCATTCCCAG CAATGTCACT AACTTGGAAG GTGGGCCTGG TCGGCAGACC ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC 120 CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA 180 GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC 240 GCCAGCCCTG TTACTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC 300 GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT 360 AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC 420 GATAAAAACC GGCGCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA 480

ATGGTGAAGT	GTGGCTCCCG	GAGAGAGAGA	TGTGGGTACC	GCCTTGTGCG	GAGACAGAGA	540
AGTGCCGACG	AGCAGCTGCA	CTGTGCCGGC	AAGGCCAAGA	GAAGTGGCGG	CCACGCGCCC	600
CGAGTGCGGG	AGCTGCTGCT	GGACGCCCTG	AGCCCCGAGC	AGCTAGTGCT	CACCCTCCTG	660
GAGGCTGAGC	CGCCCCATGT	GCTGATCAGC	CGCCCCAGTG	CGCCCTTCAC	CGAGGCCTCC	720
ATGATGATGT	CCCTGACCAA	GTTGGCCGAC	AAGGAGTTGG	TACACATGAT	CAGCTGGGCC	780
AAGAAGATTC	CCGGCTTTGT	GGAGCTCAGC	CTGTTCGACC	AAGTGCGGCT	CTTGGAGAGC	840
TGTTGGATGG	AGGTGTTAAT	GATGGGGCTG	ATGTGGCGCT	CAATTGACCA	CCCCGGCAAG	900
CTCATCTTTG	CTCCAGATCT	TGTTCTGGAC	AGGGATGAGG	GGAAATGCGT	AGAAGGAATT	960
CTGGAAATCT	TTGACATGCT	CCTGGCAACT	ACTTCAAGGT	TTCGAGAGTT	AAAACTCCAA	1020
CACAAAGAAT	ATCTCTGTGT	CAAGGCCATG	ATCCTGCTCA	ATTCCAGTAT	GTACCCTCTG	1080
GTCACAGCGA	CCCAGGATGC	TGACAGCAGC	CGGAAGCTGG	CTCACTTGCT	GAACGCCGTG	1140
ACCGATGCTT	TGGTTTGGGT	GATTGCCAAG	AGCGGCATCT	CCTCCCAGCA	GCAATCCATG	1200
CGCCTGGCTA	ACCTCCTGAT	GCTCCTGTCC	CACGTCAGGC	ATGCGAGGTG	A	1251

(2) INFORMATION FOR SEQ ID NO: 3:

5

10

15

20

30

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

	(xi)	SEQU	ENCE	E DES	SCRI	PTION	1: SE	EQ II	NO:	3:						
5	Cys 1	Ala	Val	Cys	Ser 5	Asp	Туr	Ala	Ser	Gly 10	Tyr	His	Tyr	Gly	Val 15	Trp
J	Ser	Cys	Glu	Gly 20	Cys	Lys	Ala	Phe	Phe 25	Lys	Arg	Ser	Ile	Gln 30	Gly	His
10	Asn	Asp	Tyr 35	Ile	Cys	Pro	Ala	Thr 40	Asn	Gln	Cys	Thr	Ile 45	Asp	Lys	Asn
0	Arg	Arg 50	Lys	Ser	Cys	Gln	Ala 55	Cys	Arg	Leu	Arg	Lys 60	Cys	Tyr	Glu	Val
15	Gly 65	Met														
	(2) INFO	I TAMS	ON E	OR S	EQ 1	D NC): 4:									
20	(i)	(B) (C)	LEN TYI STI	IGTH:	233 amino EDNES	Bami baci SS: s	ino a id singl	cids	i							
_25 	(ii)	MOLE	CULI	E TY	PE: 1	pept:	ide									
30	(xi)	SEQU	JENC:	E DE	SCRI	PTIO	N: S	EQ I	D N O	: 4:						
	Leu 1	Val	Leu	Thr	Leu 5	Leu	Glu	Ala	Glu	Pro 10	Pro	His	Val	Leu	Ile 15	Ser
35	Arg	Pro	Ser	Ala 20	Pro	Phe	Thr	Glu	Ala 25	Ser	Met	Met	Met	Ser 30	Leu	Thr
	Lys	Leu	Ala 35	Asp	Lys	Glu	Leu	Val 40	His	Met	Ile	Ser	Trp	Ala	Lys	Lys

	Ile	Pro 50	Gly	Phe	Val	Glu	Leu 55	Ser	Leu	Phe	Asp	Gln 60	Val	Arg	Leu	Leu
5	Glu 65	Ser	Cys	Trp	Met	Glu 70	Val	Leu	Met	Met	Gly 75	Leu	Met	Trp	Arg	Ser 80
10	Ile	Asp	His	Pro	Gly 85	Lys	Leu	Ile	Phe	Ala 90	Pro	Asp	Leu	Val	Leu 95	Asp
Õ	Arg	Asp	Glu	Gly 100	Lys	Cys	Val	Glu	Gly 105	Ile	Leu	Glu	Ile	Phe 110	Asp	Met
15	Leu	Leu	Ala 115	Thr	Thr	Ser	Arg	Phe 120	Arg	Glu	Leu	Lys	Leu 125	Gln	His	Lys
	Glu	Tyr 130	Leu	Cys	Val	Lys	Ala 135	Met	Ile	Leu	Leu	Asn 140	Ser	Ser	Met	Tyr
20	Pro 145	Leu	Val	Thr	Ala	Thr 150	Gln	Asp	Ala	Asp	Ser 155	Ser	Arg	Lys	Leu	Ala 160
20	145	Leu Leu				150					155					160
25	145 His		Leu	Asn	Ala 165	150 Val	Thr	Asp	Ala	Le u 170	155 Val	Trp	Val	Ile	Ala 175	160 Lys
25	145 His	Leu	L e u	Asn Ser 180	Ala 165 Ser	150 Val Gln	Thr Gln Arg	Asp Gln	Ala Ser 185 Ala	Leu 170 Met	155 Val Arg	Trp Leu	Val Ala	Ile Asn 190 Met	Ala 175 Leu	160 Lys Leu
25	145 His Ser	Leu Gly Leu	Leu Ile Leu 195 Asn	Asn Ser 180 Ser	Ala 165 Ser His	Val Gln Val	Thr Gln Arg	Asp Gln His 200 Asn	Ala Ser 185 Ala	Leu 170 Met	155 Val Arg	Trp Leu Lys	Val Ala Gly 205 Tyr	Ile Asn 190 Met	Ala 175 Leu Glu	160 Lys Leu

		(A)	LEN	IGTH:	477	ami a	ino a	cids	5								
		(B)	TYE	PE: a	mino	aci	id										
		(C)	STF	RANDE	DNES	SS: 5	singl	lе									
5		(D)	TOE	oroc	γ: ι	ınkno	own										
	(ii)	MOLE	ECULE	E TYP	E: F	rote	ein										
10										_							
	(xi)	SEQU	JENCE	E DES	CRIE	PTION	N: SE	EQ II	NO:	5:							
O		_	_		- 1 -	D	C	>	17-1	m L	8	T 0	C1	C1	C1	Dro	
		Asn	Tyr	ser	11e 5	Pro	Ser	Asn	vai	10	ASII	Leu	Gru	сту	15	PIO	
1.5	1				3					10					13		
15	Gly	Ara	Gln	Thr	Thr	Ser	Pro	Asn	Val	Leu	Tro	Pro	Thr	Pro	Glv	His	
	GIY	ALG	0111	20		001			25					30	4		
	Leu	Ser	Pro	Leu	Val	Val	His	Arg	Gln	Leu	Ser	His	Leu	Tyr	Ala	Glu	
20			35					40					45				
	Pro	Gln	Lys	Ser	Pro	Trp	Cys	Glu	Ala	Arg	Ser	Leu	Glu	His	Thr	Leu	
		50					55					60					
-25	Pro	Val	Asn	Arg	Glu	Thr	Leu	Lys	Arg	Lys	Val	Ser	Gly	Asn	Arg	Суз	
* was at "	65					70					75					80	
							_		_	_	_	_	- 1	•		-	
	Ala	Ser	Pro	Val		Gly	Pro	GTA	Ser		Arg	Asp	Ala	HIS		Cys	
					85					90					95		
30	21.0	V- 1	C···	505	Nen	Тиг	Ala	Ser	Glv	Tur	His	Tvr	Glv	Val	Trp	Ser	
	Ala	vai	Cys	100	ASP	ıyı	Ala	561	105		1115	- 1 -	OL J	110		DCI	
				100					100								
	Cvs	Glu	Glv	Cvs	Lvs	Ala	Phe	Phe	Lys	Arg	Ser	Ile	Gln	Gly	His	Asn	•
35	4 12		115					120					125				
	Asp	Туг	Ile	Cys	Pro	Ala	Thr	Asn	Gln	Cys	Thr	Ile	Asp	Lys	Asn	Arg	
	-	130)				135)				140	ı				

	Arg 145	Lys	Ser	Cys	Gln	Ala 150	Cys	Arg	Leu	Arg	Lys 155	Cys	Tyr	Glu	Val	Gl y 160
5	Met	Val	Lys	Cys	Gly 165	Ser	Arg	Arg	Glu	A rg 170	Cys	Gly	Tyr	Arg	Leu 175	Val
	Arg	Arg	Gln	Arg 180	Ser	Ala	Asp	Glu	Gln 185	Leu	His	Cys	Ala	Gly 190	Lys	Ala
10	Lys	Arg	Ser 195	Gly	Gly	His	Ala	Pro 200	Arg	Val	Arg	Glu	Leu 205	Leu	Leu	Asp
)	Ala	Leu 210	Ser	Pro	Glu	Gln	Leu 215	Val	Leu	Thr	Leu	Leu 220	Glu	Ala	Glu	Pro
15	Pro 225	His	Val	Leu	Ile	Ser 230	Arg	Pro	Ser	Ala	Pro 235	Phe	Thr	Glu	Ala	Ser 2 4 0
20	Met	Met	Met	Ser	Leu 2 4 5	Thr	Lys	Leu	Ala	As p 250	Lys	Glu	Leu	Val	His 255	Met
	Ile	Ser	Trp	Ala 260	Lys	Lys	Ile	Pro	Gly 265	Phe	Val	Glu	Leu	Ser 270	Leu	Phe
25	Asp	Gln	Val 275	Arg	Leu	Leu	Glu	Ser 280	Cys	Trp	Met	Glu	Val 285	Leu	Met	Met
30	Gly	Leu 290	Met	Trp	Arg	Ser	Ile 295	Asp	His	Pro	Gly	L ys 300	Leu	Ile	Phe	Ala
30	Pro 305	_	Leu	Val	Leu	Asp 310	Arg	Asp	Glu	Gly	Lys 315	Cys	Val	Glu	Gly	Ile 320
35	Leu	Glu	Ile	Phe	Asp 325		Leu	Leu	Ala	Thr 330		Ser	Arg	Phe	Arg 335	Glu
	Leu															

		Leu	Asn	Ser 355	Ser	Met	Tyr	Pro	Leu 360	Val	Thr	Ala	Thr	Gln 365	Asp	Ala	Asp
		C	G		T	T 0	N1 a	Uio	T ou	T ou	λan	λla	Val	mh	3	3 1-	T
5		ser	370	Arg	гÀг	Leu	Ala	375	Leu	ьeu	ASII	ALA	380	Thr	Asp	ALA	Leu
		Val	Trn	Val	Ile	Ala	Lvs	Ser	Glv	Ile	Ser	Ser	Gln	Gln	Gln	Ser	Met
		385		,,,,			390		1			395					400
10		Arg	Leu	Ala	Asn	Leu 405	Leu	Met	Leu	Leu	Ser	His	Val	Arg	His	Ala 415	Ser
		Asn	Lys	Gly		Glu	His	Leu	Leu		Met	Lys	Cys	Lys	Asn	Val	Val
15					420					425					430		
		Pro	Val	Tyr 435	Asp	Leu	Leu	Leu	Glu 440	Met	Leu	Asn	Ala	His	Val	Leu	Arg
		C1 ···	Cva	Lys	Sar	Sar	Tla	ሞb r	Gly	Ser	Glu	Cue	Ser	Pro	Δla	Glu	Asn
20		GIY	450	цуз	Jei	Ser	110	455	Oly	501	014	CIP	460	110	1114	Jiu	rwp
			Lys	Ser	Lys	Glu	Gly 470	Ser	Gln	Asn	Pro	Gln 475	Ser	Gln			
		465					470					4/3					
25	(2)	INFO	RMAT:	ION 1	FOR :	SEQ :	ID NO	o: 6	:								
		(i)	_	UENCI						-							
			•) TY					aCIG	5							
30) ST:					le								
		(ii)	MOL	ECUL	E TY	PE:	prot	eın									
2.5																	

Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn Leu Glu Gly Gly Pro

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

	1				5					10					15	
	Gly	Arg	Gln	Thr 20	Thr	Ser	Pro	Asn	Val 25	Leu	Trp	Pro	Thr	Pro 30	Gly	His
5	Leu	Ser	Pro 35	Leu	Val	Val	His	Arg 40	Gln	Leu	Ser	His	Leu 45	Tyr	Ala	Glu
10	Pro	Gln 50	Lys	Ser	Pro	Trp	Cys 55	Glu	Ala	Arg		Leu 60	Glu	His	Thr	Leu
>	Pro 65	Val	Asn	Arg	Glu	Thr 70	Leu	Lys	Arg	Lys	Val 75	Ser	Gly	Asn		C ys 80
15	Ala	Ser	Pro	Val	Thr 85	Gly	Pro	Gly	Ser	Lys 90	Arg	Asp	Ala		Phe 95	Cys
	Ala	Val	Cys	Ser 100	Asp	Tyr	Ala	Ser	Gly 105	Tyr	His	Tyr	Gly	Val 110	Trp	Ser
20	Cys	Glu	Gly 115	Cys	Lys	Ala	Phe	Phe 120	Lys	Arg	Ser	Ile	Gln 125	Gly	His	Asn
25	Asp	туr 130	Ile	Cys	Pro	Ala	Thr 135	Asn	Gln	Суз	Thr	Ile 140	Asp	Lys	Asn	Arg
• *	Arg 145	Lys	Ser	Cys	Gln	Ala 150	Cys	Arg	Leu	Arg	Lys 155	Cys	Туг	Glu	Val	Gly 160
30	Met	Val	Lys	Cys	Gly 165	Ser	Arg	Arg	Glu	Arg 170	Cys	Gly	Tyr	Arg	Leu 175	Val
	Arg	Arg	Gln	A rg		Ala	Asp	Glu	Gln 185		His	Cys	Ala	Gly 190		Ala
35	Lys	Arg	Ser 195		Gly	His	Ala	Pro 200		y Val	Arg	Glu	Leu 205		Leu	Asp
	Ala	Leu	ı Ser	Pro	Glu	Glr	. Leu	Val	Leu	ı Thr	Leu	Leu	Glu	ı Ala	Glu	Pro

		210					215					220				
	Pro 225	His	Val	Leu		Ser . 230	Arg	Pro	Ser	Ala	Pro 235	Phe	Thr	Glu	Ala	Ser 2 4 0
5	Met	Met	Met		Leu 2 4 5	Thr	Lys	Leu	Ala	Asp 250	Lys	Glu	Leu	Val	His 255	Met
10	Ile	Ser	Trp	Ala 260	Lys	Lys	Ile		Gl y 265	Phe	Val	Glu	Leu	Ser 270	Leu	Phe
	Asp	Gln	Val 275	Arg	Leu	Leu	Glu	Ser 280	Cys	Trp	Met	Glu	Val 285	Leu	Met	Met
15	Gly	Leu 290	Met	Trp	Arg		Ile 295	Asp	His	Pro	Gly	Lys 300	Leu	Ile	Phe	Ala
20	Pro 305	Asp	Leu	Val	Leu	Asp 310	Arg	Asp	Glu	Gly	Lys 315	Cys	Val	Glu	Gly	Ile 320
20	Leu	Glu	Ile	Phe	Asp 325	Met	Leu	Leu	Ala	Thr 330	Thr	Ser	Arg	Phe	Arg 335	Glu
25	Leu	Lys	Leu	Gln 340	His	Lys	Glu	Tyr	Leu 345	Суз	Val	Lys	Ala	Met 350	Ile	Leu
	Leu	Asn	Ser 355	Ser	Met	Tyr	Pro	Leu 360	Val	Thr	Ala	Thr	Gln 365	Asp	Ala	Asp
30	Ser	Ser 370		Lys	Leu	Ala	His 375		Leu	Asn	Ala	Val 380		Asp	Ala	Leu
35	Val		Val	Ile	Ala	Lys 390		: Gly	Ile	e Ser	395		Gln	Gln	Ser	Met 400
	Arg	g Leu	ı Ala	a Asn	105		Met	. Leu	ı Lev	1 Ser 410		s Val	Arg	g His	Ala 415	Arg

	(2) INFORMATION FOR SEQ ID NO: /:	
	(i) SEQUENCE CHARACTERISTICS:	
_	(A) LENGTH: 29 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: both	
	(D) TOPOLOGY: unknown	
10	(ii) MOLECULE TYPE: cDNA	
)		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
15	GGIGAYGARG CWTCIGGITG YCAYTAYGG	29
	(2) INFORMATION FOR SEQ ID NO: 8:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 29 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
₹5	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
30		
	AAGCCTGGSA YICKYTTIGC CCAIYTIAT	29
	(2) INFORMATION FOR SEQ ID NO: 9:	•
35	(i) SEQUENCE CHARACTERISTICS:	·
	(A) LENGTH: 22 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	

wije min was we were the

	(ii) MOLECULE TYPE: cDNA	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
	TGTTACGAAG TGGGAATGGT GA	22
10	(2) INFORMATION FOR SEQ ID NO: 10:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
25	TTGACACCAG ACCAACTGGT AATG	24
25	(2) INFORMATION FOR SEQ ID NO: 11:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 24 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	**
35		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

	GGTGGCGACG ACTCCTGGAG CCCG	24
	(2) INFORMATION FOR SEQ ID NO: 12:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 22 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
10	(D) TOPOLOGY: linear	
٠.	(ii) MOLECULE TYPE: cDNA	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
	GTACACTGAT TTGTAGCTGG AC	22
20	(2) INFORMATION FOR SEQ ID NO: 13:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
	CCATGATGAT GTCCCTGACC	20
35	(2) INFORMATION FOR SEQ ID NO: 14:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
10	TCGCATGCCT GACGTGGGAC	20
ar de la companya de	(2) INFORMATION FOR SEQ ID NO: 15:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20	(ii) MOLECULE TYPE: cDNA	
, Ç, 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
•	GGCSTCCAGC ATCTCCAGSA RCAG	24
	(2) INFORMATION FOR SEQ ID NO: 16:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	•
35	(ii) MOLECULE TYPE: cDNA	
	(TT) FIOHEOUTH TIED: COME	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:	
	GGAAGCTGGC TCACTTGCTG	20
5	(2) INFORMATION FOR SEQ ID NO: 17:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 base pairs (B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
	TCTTGTTCTG GACAGGGATG	20
20	(2) INFORMATION FOR SEQ ID NO: 18:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
35	GCATGGAACA TCTGCTCAAC	20
	(2) INFORMATION FOR SEQ ID NO: 19:	
	(2) Intolumiton for any 12 no. 15.	

(A) LENGTH: 21 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
5		
	(ii) MOLECULE TYPE: cDNA	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
	AGCAAGTTCA GCCTGTTAAG T	21
	(2) INFORMATION FOR SEQ ID NO: 20:	
15		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1257 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
25		
•	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
	ATGAATTACA GCATTCCCAG CAATGTCACT AACTTGGAAG GTGGGCCTGG TCGGCAGACC	60
30	ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC	120
	CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA	180
	GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC	_240
35	arionaliser mesicinal analogical of diagrams and mesicinal and arionalise	J 240
	GCCAGCCCTG TTACTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC	300
	GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT	360

AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC 420 GATAAAAACC GGCGCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA 480 ATGGTGAAGT GTGGCTCCCG GAGAGAGAGA TGTGGGTACC GCCTTGTGCG GAGACAGAGA 540 AGTGCCGACG AGCAGCTGCA CTGTGCCGGC AAGGCCAAGA GAAGTGGCGG CCACGCGCCC 600 CGAGTGCGGG AGCTGCTGCT GGACGCCCTG AGCCCCGAGC AGCTAGTGCT CACCCTCCTG 660 GAGGCTGAGC CGCCCCATGT GCTGATCAGC CGCCCCAGTG CGCCCTTCAC CGAGGCCTCC 720 ATGATGATGT CCCTGACCAA GTTGGCCGAC AAGGAGTTGG TACACATGAT CAGCTGGGCC 780 AAGAAGATTC CCGGCTTTGT GGAGCTCAGC CTGTTCGACC AAGTGCGGCT CTTGGAGAGC 840 TGTTGGATGG AGGTGTTAAT GATGGGGCTG ATGTGGCGCT CAATTGACCA CCCCGGCAAG 900 CTCATCTTTG CTCCAGATCT TGTTCTGGAC AGGGATGAGG GGAAATGCGT AGAAGGAATT 960 CTGGAAATCT TTGACATGCT CCTGGCAACT ACTTCAAGGT TTCGAGAGTT AAAACTCCAA 1020 CACAAAGAAT ATCTCTGTGT CAAGGCCATG ATCCTGCTCA ATTCCAGTAT GTACCCTCTG 1080 GTCACAGCGA CCCAGGATGC TGACAGCAGC CGGAAGCTGG CTCACTTGCT GAACGCCGTG 1140 ACCGATGCTT TGGTTTGGGT GATTGCCAAG AGCGGCATCT CCTCCCAGCA GCAATCCATG 1200 CGCCTGGCTA ACCTCCTGAT GCTCCTGTCC CACGTCAGGC ATGCGAGGTC TGCCTGA 1257

(2) INFORMATION FOR SEQ ID NO: 21:

10

15

20

.25

30

35

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

	(xi)	SEQ	JENCI	E DES	SCRI	PTIO	V: SI	EQ II	ON C	: 21	:						
5	W-+	3	П	G	T1-	D	C	3	v- 1	mL	7 a m	T	C1	C1	C1	D	
	met 1	ASN	TYE	ser	5	Pro	ser	ASI	Val	10	ASII	Leu	GIU	Gly	15	Pro	
		_						_		_	_	_		_			
10	Gly	Arg	Gln	Thr 20	Thr	Ser	Pro	Asn	Val 25	Leu	Trp	Pro	Thr	Pro 30	GTA	His	
	Leu	Ser	Pro 35	Leu	Val	Val	His	Arg 40	Gln	Leu	Ser	His	Leu 45	Tyr	Ala	Glu	
15	Pro	Gln 50	Lys	Ser	Pro	Trp	Cys 55	Glu	Ala	Arg	Ser	Leu 60	Glu	His	Thr	Leu	
	Pro 65	Val	Asn	Arg	Glu	Thr 70	Leu	Lys	Arg	Lys	Val 75	Ser	Gly	Asn	Arg	C ys 80	
20																	
	Ala	Ser	Pro	Val	Thr 85	Gly	Pro	Gly	Ser	Lys 90	Arg	Asp	Ala	His	Ph e 95	Сув	
					03					70					,,,		
25	Ala	Val	Cys		Asp	Tyr	Ala	Ser		Tyr	His	Tyr	Gly	Val	Trp	Ser	
25 				100					105					110			
	Cys	Glu		Cys	Lys	Ala	Phe		Lys	Arg	Ser	Ile		Gly	His	Asn	
			115					120					125				
30	Asp		Ile	Cys	Pro	Ala		Asn	Gln	Cys	Thr		Asp	Lys	Asn	Arg	
		130					135					140					
	-	Lys	Ser	Cys	Gln		Cys	Arg	Leu	Arg			Tyr	Glu	Val		
35	145					150					155					160	
	Met	Val	Lys	Cys	Gly	Ser	Arg	Arg	Glu	Arg	Cys	Gly	Tyr	Arg	Leu	Val	
					165					170					175		
	Arg	Arg	Gln	Arg	Ser	Ala	Asp	Glu	Gln	Leu	His	Cys	Ala	Gly	Lys	Ala	

				180					185					190		
	Lys	Arg	Ser 195	Gly	Gly	His		Pro 200	Arg	Val	Arg	Glu	Leu 205	Leu	Leu	Asp
5	Ala	Leu 210	Ser	Pro	Glu	Gln	Leu 215	Val	Leu	Thr		Leu 220	Glu	Ala	Glu	Pro
10	Pro 225	His	Val	Leu	Ile	Ser 230	Arg	Pro	Ser	Ala	Pro 235	Phe	Thr	Glu	Ala	Ser 2 4 0
)	Met	Met	Met	Ser	Leu 245	Thr	Lys	Leu	Ala	As p 250	Lys	Glu	Leu	Val	His 255	Met
15	Ile	Ser	Trp	Ala 260	Lys	Lys	Ile	Pro	Gly 265	Phe	Val	Glu	Leu	Ser 270	Leu	Phe
	Asp	Gln	Val 275	Arg	Leu	Leu	Glu	Ser 280	Cys	Trp	Met	Glu	Val 285	Leu	Met	Met
20	Gly	Leu 290		Trp	Arg	Ser	Ile 295	Asp	His	Pro	Gly	Lys 300	Leu	Ile	Phe	Ala
25	Pro 305		Leu	Val	Leu	Asp 310	Arg	Asp	Glu	Gly	Lys 315	Cys	Val	Glu	Gly	11e 320
	Leu	Glu	Ile	Phe	Asp 325	Met	Leu	Leu	Ala	Thr 330		Ser	Arg	Phe	Arg 335	Glu
30	Leu	Lys	Leu	Gln 340	His	Lys	Glu	Tyr	Leu 345		Val	Lys	Ala	Met 350		Leu
	Lev	ı Asr	355		. Met	Туг	Pro) Leu 360		Thr	: Ala	Thi	Gln 365		Ala	Asp
35	Sei	r Sei	r Arq	g Ly:	s Lei	ı Ala	a His	s Lev	ı Lev	ı Ası	n Ala	a Vai	l Thi	Asp	Ala	ı Leı

Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser Gln Gln Gln Ser Met

370

400

390

385

Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His Val Arg His Ala Arg 405 410 Ser Ala (2) INFORMATION FOR SEQ ID NO: 22: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 15 (ii) MOLECULE TYPE: cDNA 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22: 34 CTTGGATCCA TAGCCCTGCT GTGATGAATT ACAG (2) INFORMATION FOR SEQ ID NO: 23: _ 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single 30 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23: 33 GATGGATCCT CACCTCAGGG CCAGGCGTCA CTG

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1898 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

10

15

20

_25

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CACGAATCTT TGAGAACATT ATAATGACCT TTGTGCCTCT TCTTGCAAGG TGTTTTCTCA 60 GCTGTTATCT CAAGACATGG ATATAAAAAA CTCACCATCT AGCCTTAATT CTCCTTCCTC 120 CTACAACTGC AGTCAATCCA TCTTACCCCT GGAGCACGGC TCCATATACA TACCTTCCTC 180 CTATGTAGAC AGCCACCATG AATATCCAGC CATGACATTC TATAGCCCTG CTGTGATGAA 240 TTACAGCATT CCCAGCAATG TCACTAACTT GGAAGGTGGG CCTGGTCGGC AGACCACAAG 300 CCCAAATGTG TTGTGGCCAA CACCTGGGCA CCTTTCTCCT TTAGTGGTCC ATCGCCAGTT 360 ATCACATCTG TATGCGGAAC CTCAAAAGAG TCCCTGGTGT GAAGCAAGAT CGCTAGAACA 420 CACCTTACCT GTAAACAGAG AGACACTGAA AAGGAAGGTT AGTGGGAACC GTTGCGCCAG 480 CCCTGTTACT GGTCCAGGTT CAAAGAGGGA TGCTCACTTC TGCGCTGTCT GCAGCGATTA 540 CGCATCGGGA TATCACTATG GAGTCTGGTC GTGTGAAGGA TGTAAGGCCT TTTTTAAAAG 600 AAGCATTCAA GGACATAATG ATTATATTTG TCCAGCTACA AATCAGTGTA CAATCGATAA 660 AAACCGGCGC AAGAGCTGCC AGGCCTGCCG ACTTCGGAAG TGTTACGAAG TGGGAATGGT 720

GAAGTGTGGC TCCCGGAGAG AGAGATGTGG GTACCGCCTT GTGCGGAGAC AGAGAAGTGC 780 CGACGAGCAG CTGCACTGTG CCGGCAAGGC CAAGAGAAGT GGCGGCCACG CGCCCCGAGT 840 GCGGGAGCTG CTGCTGGACG CCCTGAGCCC CGAGCAGCTA GTGCTCACCC TCCTGGAGGC 900 TGAGCCGCCC CATGTGCTGA TCAGCCGCCC CAGTGCGCCC TTCACCGAGG CCTCCATGAT 960 GATGTCCCTG ACCAAGTTGG CCGACAAGGA GTTGGTACAC ATGATCAGCT GGGCCAAGAA 1020 GATTCCCGGC TTTGTGGAGC TCAGCCTGTT CGACCAAGTG CGGCTCTTGG AGAGCTGTTG 1080 GATGGAGGTG TTAATGATGG GGCTGATGTG GCGCTCAATT GACCACCCCG GCAAGCTCAT 1140 CTTTGCTCCA GATCTTGTTC TGGACAGGGA TGAGGGGAAA TGCGTAGAAG GAATTCTGGA 1200 AATCTTTGAC ATGCTCCTGG CAACTACTTC AAGGTTTCGA GAGTTAAAAC TCCAACACAA 1260 AGAATATCTC TGTGTCAAGG CCATGATCCT GCTCAATTCC AGTATGTACC CTCTGGTCAC 1320 AGCGACCCAG GATGCTGACA GCAGCCGGAA GCTGGCTCAC TTGCTGAACG CCGTGACCGA 1380 TGCTTTGGTT TGGGTGATTG CCAAGAGCGG CATCTCCTCC CAGCAGCAAT CCATGCGCCT 1440 GGCTAACCTC CTGATGCTCC TGTCCCACGT CAGGCATGCG AGTAACAAGG GCATGGAACA 1500 TCTGCTCAAC ATGAAGTGCA AAAATGTGGT CCCAGTGTAT GACCTGCTGC TGGAGATGCT 1560 GAATGCCCAC GTGCTTCGCG GGTGCAAGTC CTCCATCACG GGGTCCGAGT GCAGCCCGGC 1620 AGAGGACAGT AAAAGCAAAG AGGGCTCCCA GAACCCACAG TCTCAGTGAC GCCTGGCCCT 1680 GAGGTGAACT GGCCCACAGA GGTCACAAGC TGAAGCGTGA ACTCCAGTGT GTCAGGAGCC 1740 TGGGCTTCAT CTTTCTGCTG TGTGGTCCCT CATTTGGTGA TGGCAGGCTT GGTCATGTAC 1800 CATCCTTCCC TCCACCTTCC CAACTCTCAG GAGTCGGTGT GAGGAAGCCA TAGTTTCCCT 1860

 \bigcirc

15

10

5

20

- ,25

30

	TGTTAGCAG	GA GG	GACA	ATTTG	TAA 3	CGAG	CGT	TTCC	ACAC								1898
	(2) INFO	RMATI	ON E	FOR S	SEQ I	D NC): 25	ō:									
5	(i)	(B)	LEN TYI STI	IGTH: PE: a	ARACT 530 amino EDNES	ami aci SS: s	.no a .d singl	cids	:								
10	(ii)	MOLE	CULE	E TYP	e: p	epti	.de										
15	(xi)	SEQU	JENCE	E DES	SCRIF	TION	ı: SE	EQ II	NO:	25:							
20	Met 1	Asp	Ile	Lys	Asn 5	Ser	Pro	Ser	Ser	Leu 10	Asn	Ser	Pro	Ser	Ser 15	Tyr	
20	Asn	Cys	Ser	Gln 20	Ser	Ile	Leu	Pro	Leu 25	Glu	His	Gly	Ser	Ile 30	Tyr	Ile	
25	Pro	Ser	Ser 35	Tyr	Val	Asp	Ser	His 40	His	Glu	туг	Pro	Ala 45	Met	Thr	Phe	
	Tyr	Ser 50	Pro	Ala	Val	Met	As n 55	Tyr	Ser	Ile	Pro	Ser 60	Asn	Val	Thr	Asn	
30	Leu 65	Glu	Gly	Gly	Pro	Gly 70	Arg	Gln	Thr	Thr	Ser 75	Pro	Asn	Val	Leu	Trp 80	
	Pro	Thr	Pro	Gly	His	Leu	Ser	Pro	Leu	Val 90	Val	His	Arg	Gln	Leu 95	Ser	•

Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val

His Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser 105

100

110

5	Ser	Gly 130	Asn	Arg	Cys	Ala	Ser 135	Pro	Val	Thr	Gly	Pro 140	Gly	Ser	Lys	Arg
J	Asp 145	Ala	His	Phe	Cys	Ala 150	Val	Cys	Ser	Asp	Туг 155	Ala	Ser	Gly	Tyr	His 160
10	Tyr	Gly	Val	Trp	Ser 165	Cys	Glu	Gly	Cys	Lys 170	Ala	Phe	Phe	Lys	Arg 175	Ser
`	Ile	Gln	Gly	His 180	Asn	Asp	Tyr	Ile	Cys 185	Pro	Ala	Thr	Asn	Gln 190	Cys	Thr
15	Ile	Asp	Lys 195	Asn	Arg	Arg	Lys	Ser 200	Cys	Gln	Ala	Cys	Arg 205	Leu	Arg	Lys
	Cys	Туг 210	Glu	Val	Gly	Met	Val 215	Lys	Cys	Gly	Ser	Arg 220	Arg	Glu	Arg	Суз
20	~1	_	_	_			•	a 1	3	C	21.	Aan	Gl v	Gln	ī.eu	His
	G1y 225	Tyr	Arg	Leu	Val	230	Arg	GIN	ALG	ser	235	Asp	GIU	GIII	Deu	240
_2,5	225					230	Arg				235					240
. 25	225 Cys	Ala	Gly	Lys	Ala 245 Asp	230 Lys		Ser	Gly	Gly 250	235 His	Ala	Pro	Arg	Val 255	240 Arg
	225 Cys Glu	Ala Leu	Gly Leu	Lys Leu 260	Ala 245 Asp	230 Lys Ala	Arg	Ser	Gly Pro 265	Gly 250 Glu	235 His	Ala Leu	Pro Val	Arg Leu 270	Val 255	240 Arg Leu
	225 Cys Glu Leu	Ala Leu Glu	Gly Leu Ala 275	Lys Leu 260 Glu	Ala 245 Asp	Lys Ala	Arg Leu His	Ser Ser Val 280	Gly Pro 265 Leu	Gly 250 Glu Ile	235 His Gln Ser	Ala Leu Arg	Pro Val Pro 285	Arg Leu 270 Ser	Val 255 Thr	240 Arg Leu
	225 Cys Glu Leu	Ala Leu Glu Thr 290 Leu	Gly Leu Ala 275 Glu	Leu 260 Glu	Ala 245 Asp Pro	Lys Ala Pro	Arg Leu His Met 295	Ser Ser Val 280	Gly Pro 265 Leu Ser	Gly 250 Glu Ile	235 His Gln Ser	Ala Leu Arg Lys 300	Pro Val Pro 285	Arg Leu 270 Ser	Val 255 Thr Ala Asp	240 Arg Leu Pro

					325					330					335	
5	Glu	Val	Leu	Met 340	Met	Gly	Leu	Met	Trp 345	Arg	Ser	Ile	Asp	His 350	Pro	Gly
J	Lys	Leu	Ile 355	Phe	Ala	Pro	Asp	Leu 360	Val	Leu	Asp	Arg	Asp 365	Glu	Gly	Lys
10	Cys	Val 370	Glu	Gly	Ile	Leu	Glu 375	Ile	Phe	Asp	Met	Leu 380	Leu	Ala	Thr	Thr
9	Ser 385	Arg	Phe	Arg	Glu	Leu 390	Lys	Leu	Gln	His	Lys 395	Glu	Tyr	Leu	Cys	Val 400
15	Lys	Ala	Met	Ile	Leu 405	Leu	Asn	Ser	Ser	Met 410	Tyr	Pro	Leu	Val	Thr 415	Ala
	Thr	Gln	Aen	Δla	Asp	Ser	Ser	Ara	T.vs	T.e.u	Δla	His	Leu	T.en	Asn	Ala
20		0111	rap	420				g	425	Deu	rua.		204	430		
20			Asp 435	420	_				425					430		
25	Val	Thr	Asp	420 Ala	Leu	Val	Trp	Val 440	425	Ala	Lys	Ser	Gly 445	430 Ile	Ser	Ser
25	Val Gln	Thr Gln 450	Asp 435	420 Ala Ser	Leu Met	Val	Trp Leu 455	Val 440 Ala	425 Ile Asn	Ala Leu	Lys Leu	Ser Met 460	Gly 445 Leu	430 Ile Leu	Ser	Ser His
25	Val Gln Val 465	Thr Gln 450 Arg	Asp 435 Gln	420 Ala Ser Ala	Leu Met	Val Arg Asn 470	Trp Leu 455 Lys	Val 440 Ala	425 Ile Asn Met	Ala Leu Glu	Lys Leu His 475	Ser Met 460 Leu	Gly 445 Leu Leu	430 Ile Leu Asn	Ser Ser Met	Ser His Lys 480
25	Val Gln Val 465	Thr Gln 450 Arg	Asp 435 Gln His	420 Ala Ser Ala Val	Leu Met Ser Val 485	Val Arg Asn 470 Pro	Trp Leu 455 Lys Val	Val 440 Ala Gly	425 Ile Asn Met	Ala Leu Glu Leu 490	Lys Leu His 475 Leu	Ser Met 460 Leu	Gly 445 Leu Leu	430 Ile Leu Asn Met	Ser Ser Met Leu 495	Ser His Lys 480 Asn

525

Ser Gln

	(2) INFORMATION FOR SEQ ID NO: 26:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: other nucleic acid	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:	
	GTGCGGATCC TCTCAAGACA TGGATATAAA	30
20	(2) INFORMATION FOR SEQ ID NO: 27:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 25 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:	•
35	AGTAACAGGG CTGGCGCAAC GGTTC	25
	(2) INFORMATION FOR SEQ ID NO: 28:	

(A)	LENGTH	: 22	base	pair
(B)	TYPE:	nucle	eic a	cid
(C)	STRAND	EDNE	SS: s:	ingle

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ACTGGCGATG GACCACTAAA GG

15

10